Central Valley Chinook Genetics Update

There are several genetic investigations on Central Valley Chinook; some past, some present. This is an update on just one of those genetic investigations; by Dr. Hedgecock formerly at UC Davis, Bodega Marine Laboratory, and Dr. Mike Banks, currently at Oregon State University, Hatfield Marine Science Center.

DWR started this project about 10 years ago. At that time, the Chinook emphasis was on winter run, but over time that has shifted to spring run. Although there may be an emphasis on one Chinook population or another over time, the researchers develop new information for all the populations. For instance, while searching for spring run markers, Dr. Banks developed more powerful markers for winter run, and fall and late-fall runs.

There are three tasks in this research; population structure, population composition of unknowns, and identification of unknown individuals. Population structure is an analysis of the genetic relatedness of populations of known origin. Population composition of unknowns is an analysis of the genetic information from the baselines of known origin, and the genetic information from a mixed group of unknown origin, to estimate the baseline populations in that unknown group. A common name for this is Mixed Stock Analysis. The researchers of this investigation took it one step further to try to estimate the identity of individuals in a mixed group of unknowns.

Towards the end of the "winter run"-phase of this project, in 2000, we had geneticists, from California and Washington, that were working on Central Valley Chinook genetics, meet to discuss whether the results were ready to put to management use. The answer was yes, for winter run.

Figure 1 is the population structure of Central Valley Chinook based on the genetic markers and the baseline at the end of the "winter run" phase of the research (Banks, 2000). Winter run is very distinct and the most distinct of the populations. Butte spring run is a separate population from Mill and Deer spring run, and fall run and late-fall run are distinct at the population structure level. Although not explicit in Figure 1, the hatchery Chinook are in the fall-run segment of the tree. The x axis is the genetic distance among the populations. The distances are based on microsatellite DNA, and are still only a relative difference, not an absolute. Professionals are still discussing the genetic distances based on microsatellites relative to that based on proteins in the scientific literature.

The other goal of the investigation was to use baseline data to predict populations in a mixture of unknowns; such as adults in the ocean, or juveniles in the Delta. The prediction is only as good as the baseline. In the case of the population structure, missing populations can be added without affecting the existing structure. In the case of predicting populations in a mixture of unknowns, missing populations can affect the results. That was a point of discussion at the meeting of geneticists in 2000. At the end of the day they all agreed that, because winter run was so distinct, missing populations in the baseline wouldn't effect winter run identification in mixtures of unknowns.

Figures 2 and 3 are the result of applying the winter-run markers to mixed populations of juvenile Chinook of unknown origin at the Delta export facilities from 1995/96 through 2001/02. Figure 2 is an aggregated view of the data, and Figure 3 is an annual view of the data. Based on the results, the fish management biologists changed their working hypothesis on how winter run arrived at the export facilities. The former hypothesis was winter run would arrive at the exports from October through May, with a peak from February through April, at a length defined by emergence and an empirical growth rate. The revised hypothesis, based on genetics, is genetic winter run arrive at the exports at a surprisingly similar length, with a peak between mid February and mid April. Over the seven years, most of the genetic winter run were within the winter run length range, but only about half the Chinook in the winter run length range were genetic winter run (Figure 2). Among the seven years, there was quite a bit of seasonal variability (Figure 3).

One of the management uses genetic identification is estimating winter run mortality at the Delta export facilities. The mortality, called loss, isn't exactly proportional to the number salvage because the mortality factors at each facility are different. Figure 4 is the loss based on genetic characterization and length criteria. The loss based on genetics varies from 20% to 78% of that based on length criteria. The highest percentage genetic loss occurred in 2001, the year of the highest genetic winter run loss. There are different ways of averaging this information, but a rule of thumb is the genetic loss is about half of the length criteria loss, and it varies a lot.

DWR still funds genetic investigations, and the emphasis is on spring run now. Much of the research has been on finding new markers for spring run. We have settled on 12 markers that identify both spring run and winter run in one laboratory assay. Some of the new markers for spring run are more powerful for winter than the old winter run markers. Of the twelve markers for spring and winter runs, and the 7 older markers for winter run, only three are in common (Table 1).

Figure 5 is a factorial analysis with the 12 spring and winter run markers. Winter run isn't on this version of the analysis because it is so distinct that the other populations would be too compressed to see their separation. The yellow and blue dots are Butte and Mill/Deer creeks spring run, and the black and gray dots are the fall and late fall.

Table 2 is the modeled accuracy of the individual identification with the 12 spring run markers. The researcher sequentially removed one sample from the baseline and estimated its identity from the rest of the baseline. All the populations have high accuracy, but the individual values for winter and spring are high compared to the low values for fall and late fall, therefore missing populations in the baseline may effect our ability to identify fall and late fall in mixed populations.

In the new contract with Dr. Banks, we are investigating more spring run issues, such as the Feather River spring run, which has not been brought into the baseline yet, and other

newer phenotypically spring-run like populations developing in the upper Sacramento River.

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